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100

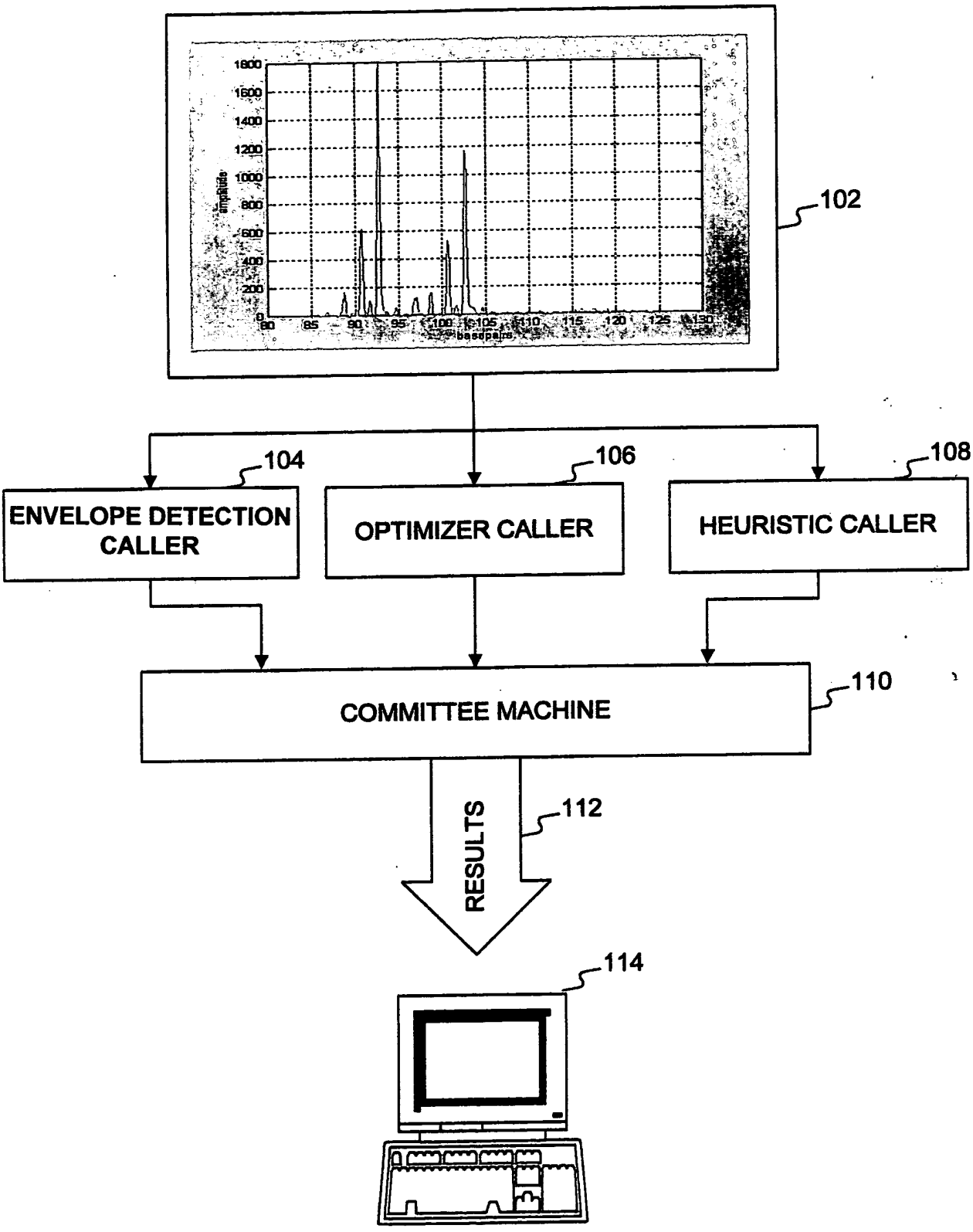

Fig. 1

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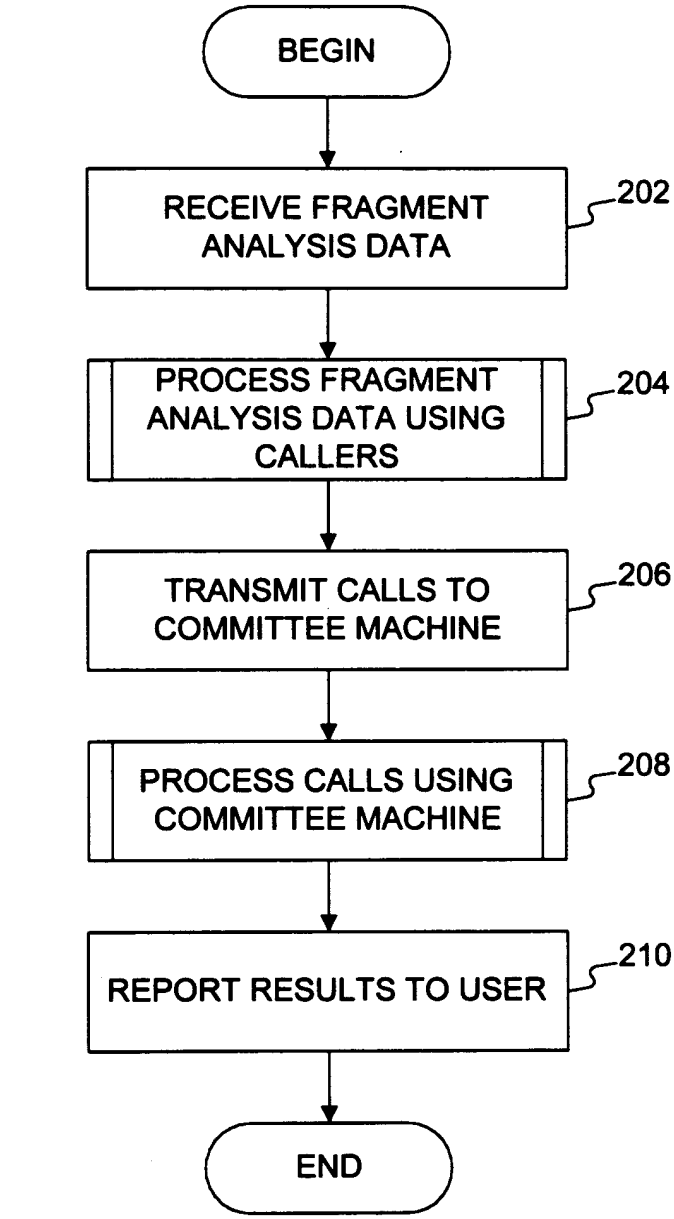

Fig. 2

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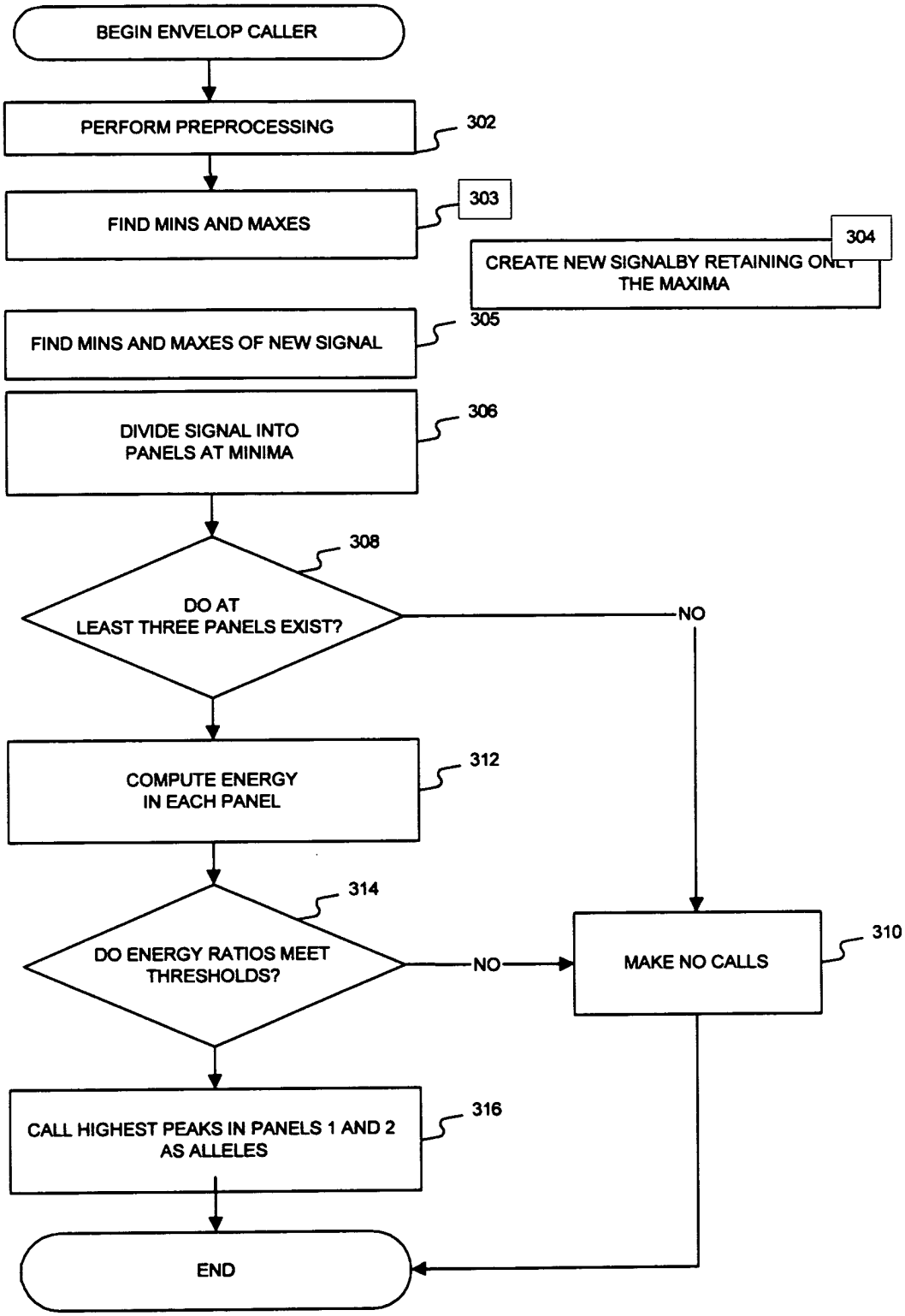

Fig. 3A

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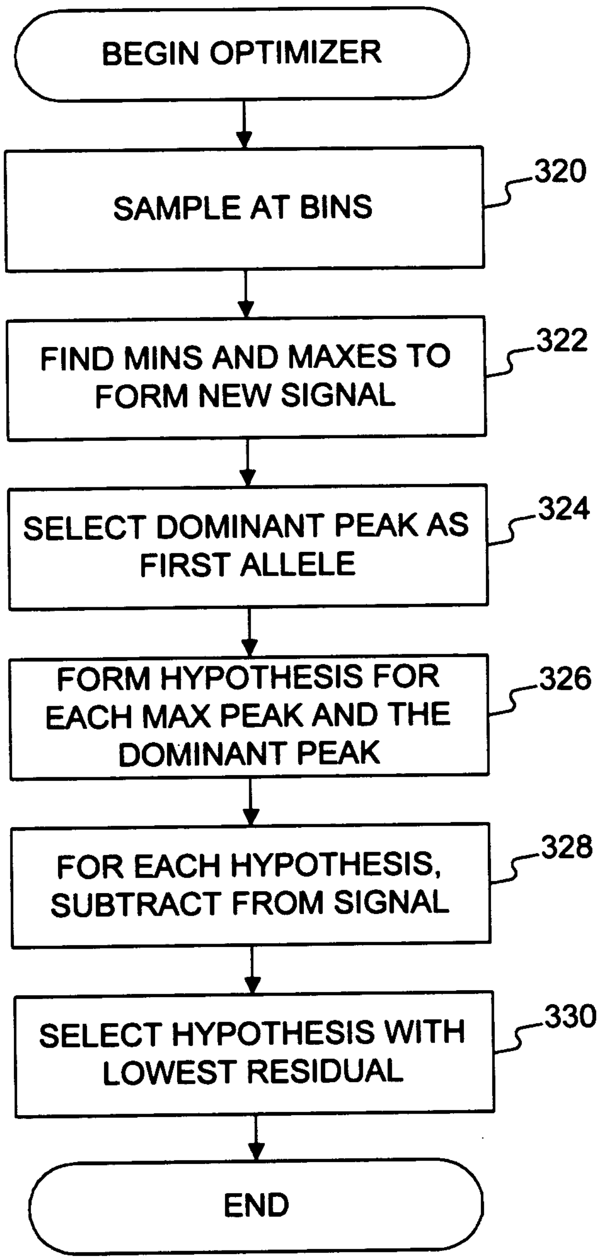

Fig. 3B

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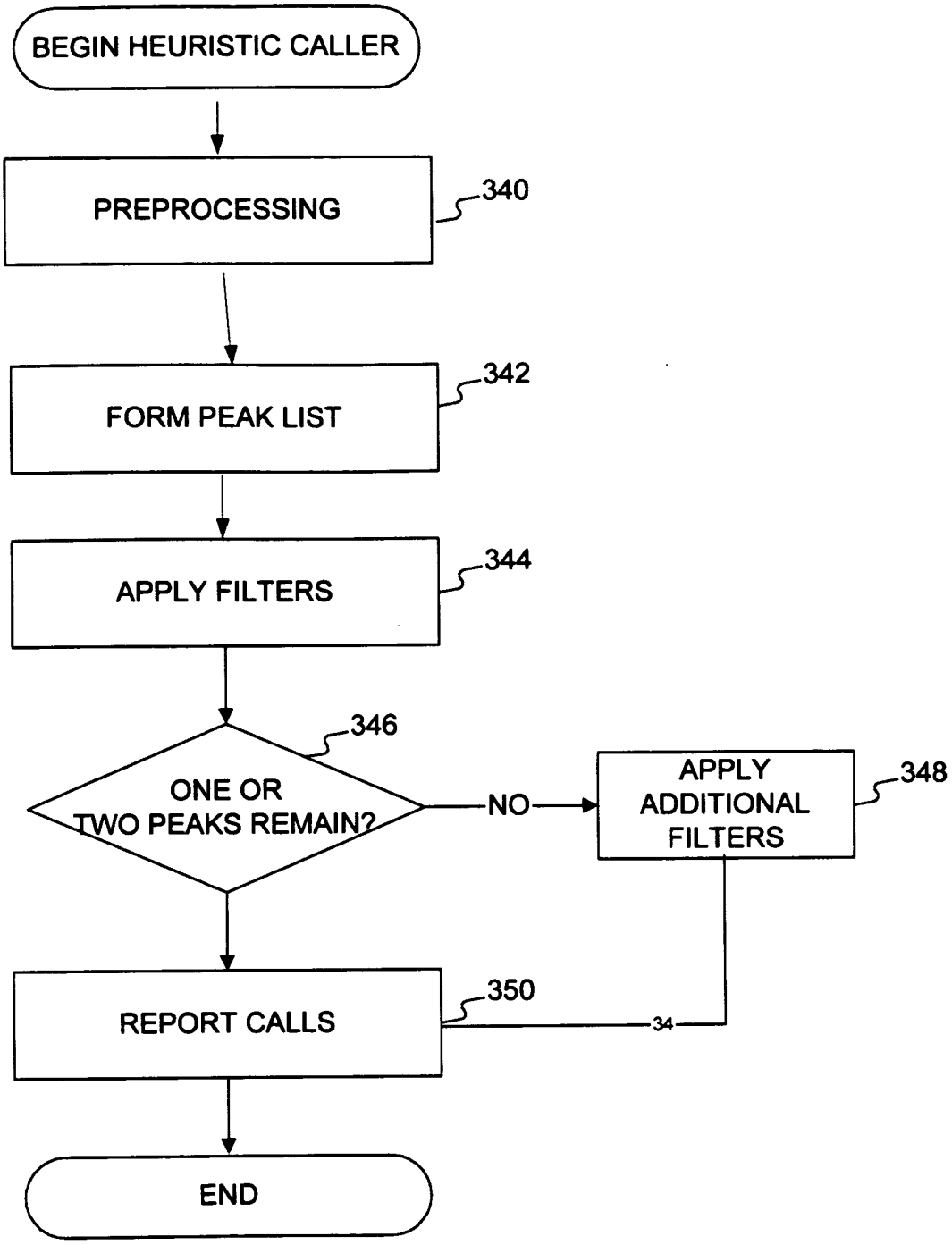

Fig. 3C

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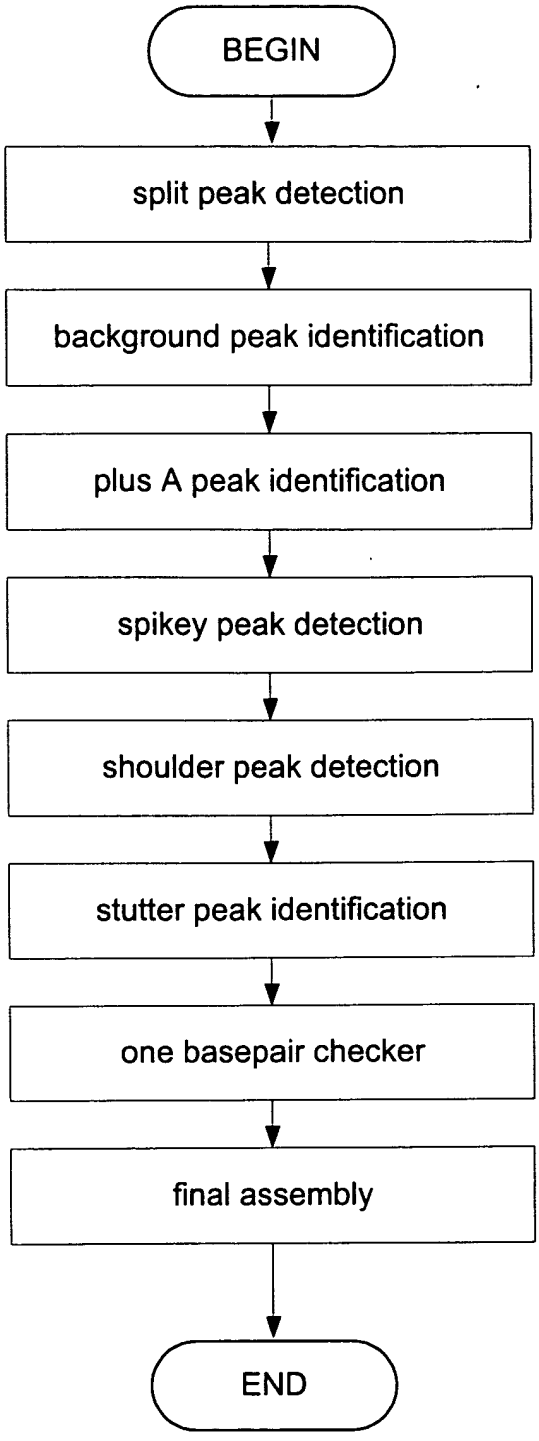

D6S474 D6S1043

Fig. 3D

APPROVED BY DRAFTSMAN | O.G. FIG. | CLASS | SUBCLASS

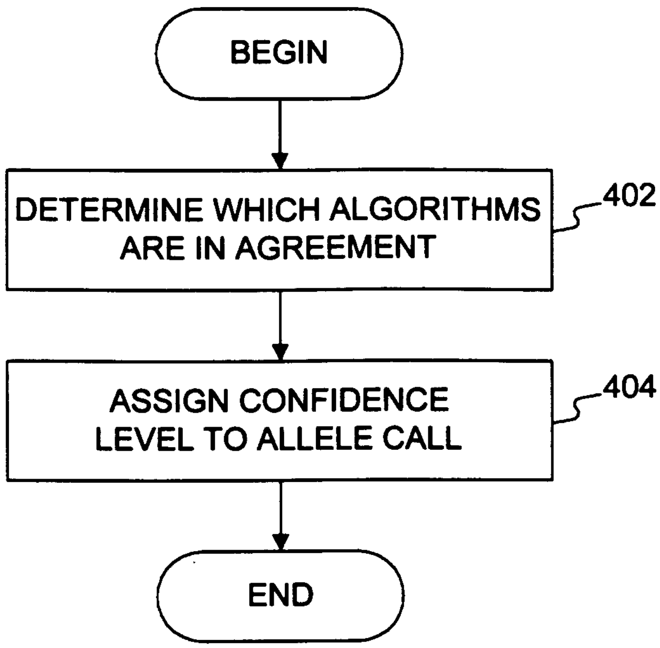

Fig. 4

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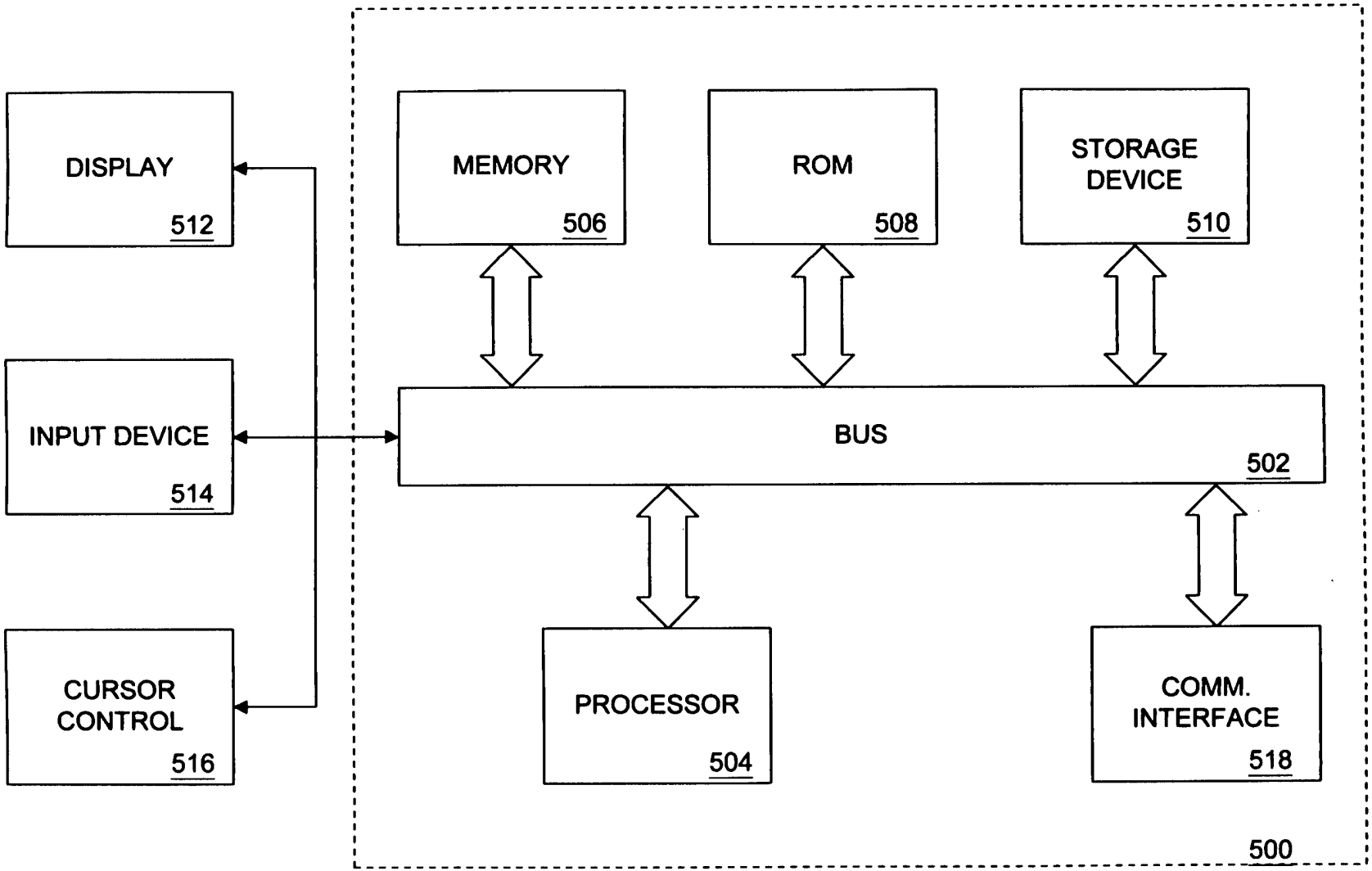

Fig. 5

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	CLASS	SUBCLASS

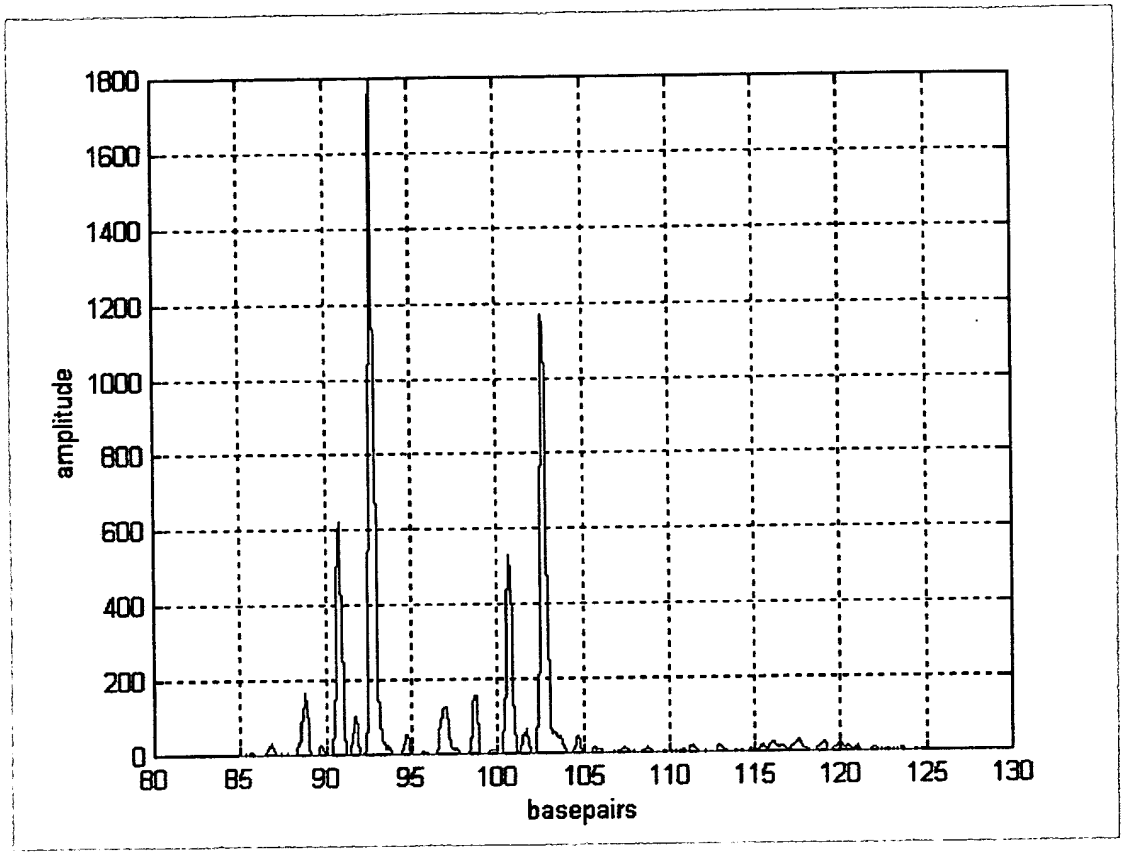

Figure 6

APPROVED BY DRAFTSMAN	O G. FIG.	
	CLASS	SUBCLASS

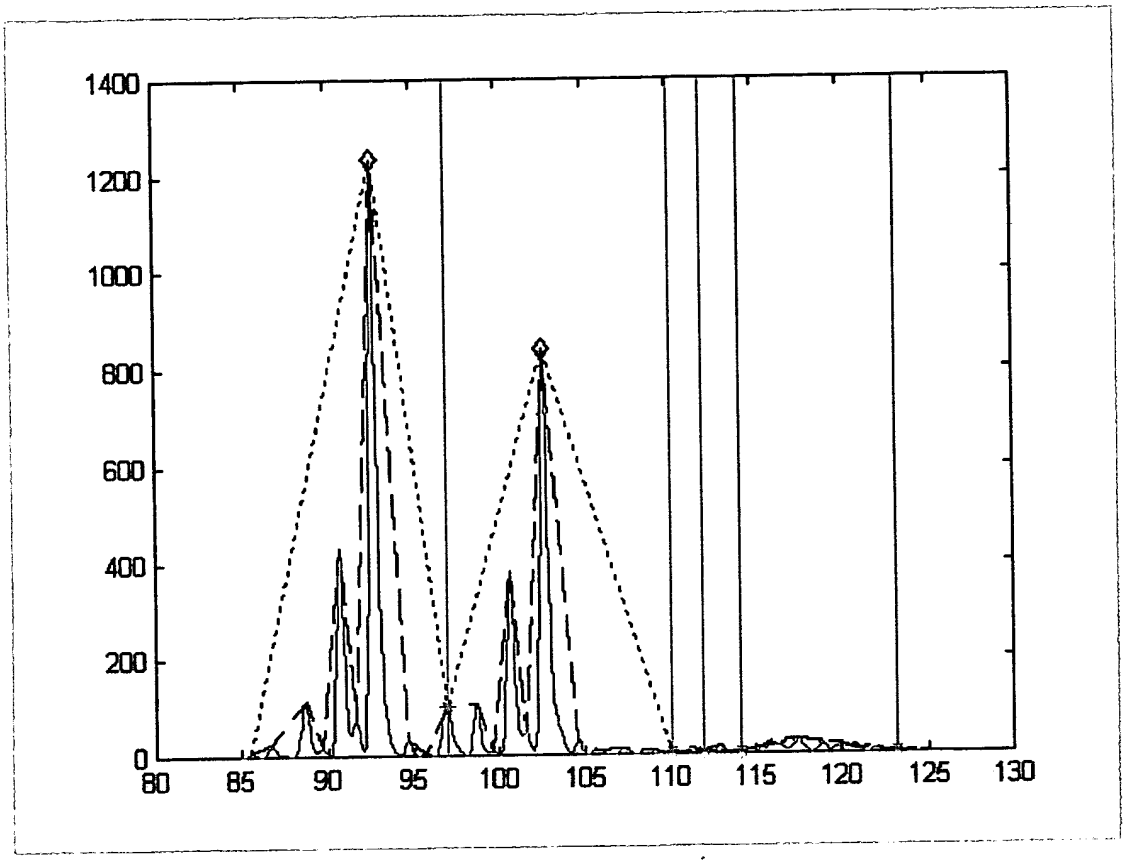

Figure 7

APPROVED BY DRAFTSMAN | O.G. FIG. | CLASS | SUBCLASS

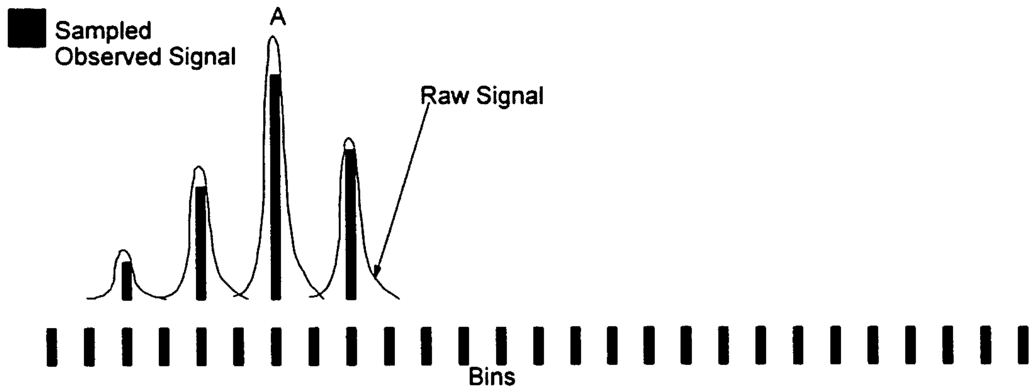

Figure 8

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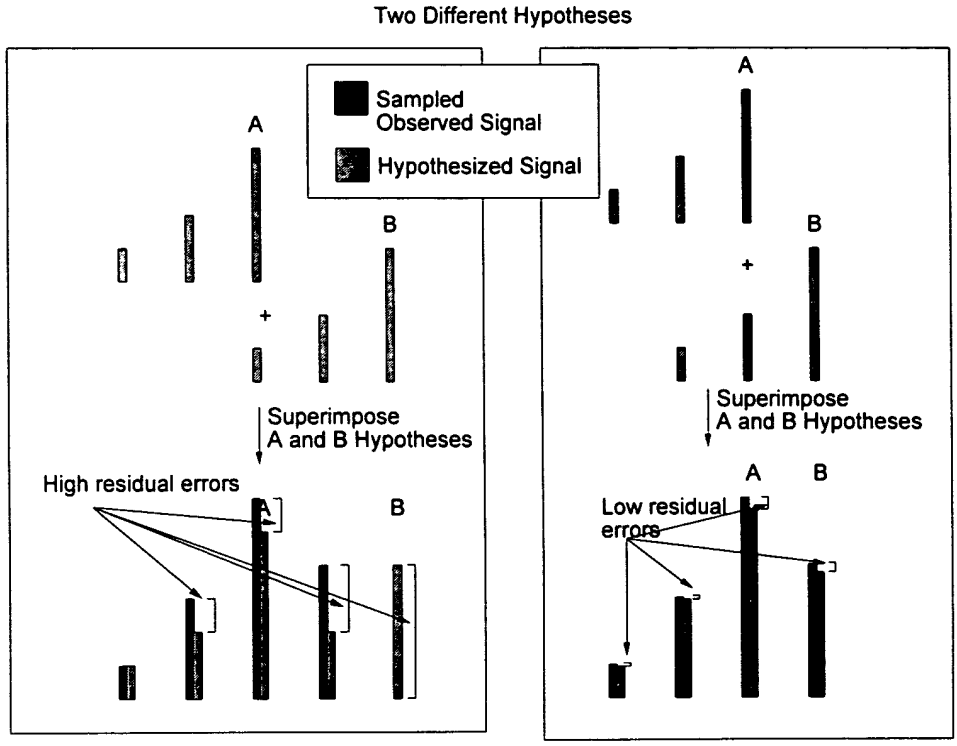

Figure 9

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	CLASS	SUBCLASS

Allele Calling for di-nucleotide marker in linkage mapping application Sample Data (3)

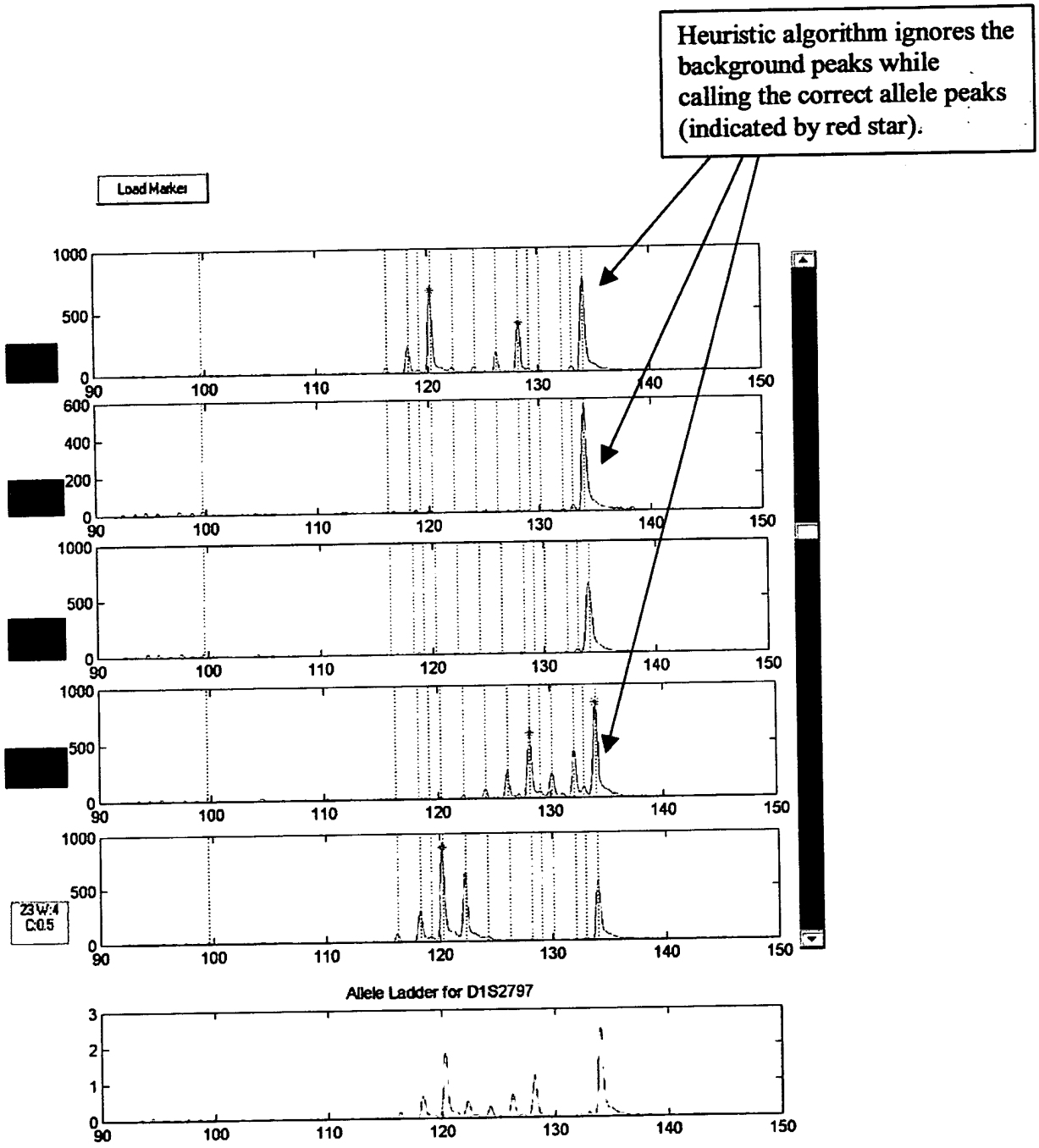

Figure 10

APPROVED BY DRAFTSMAN	O G. FIG.	
	CLASS	SUBCLASS

Allele Calling for di-nucleotide marker in linkage mapping application Sample Data (2)

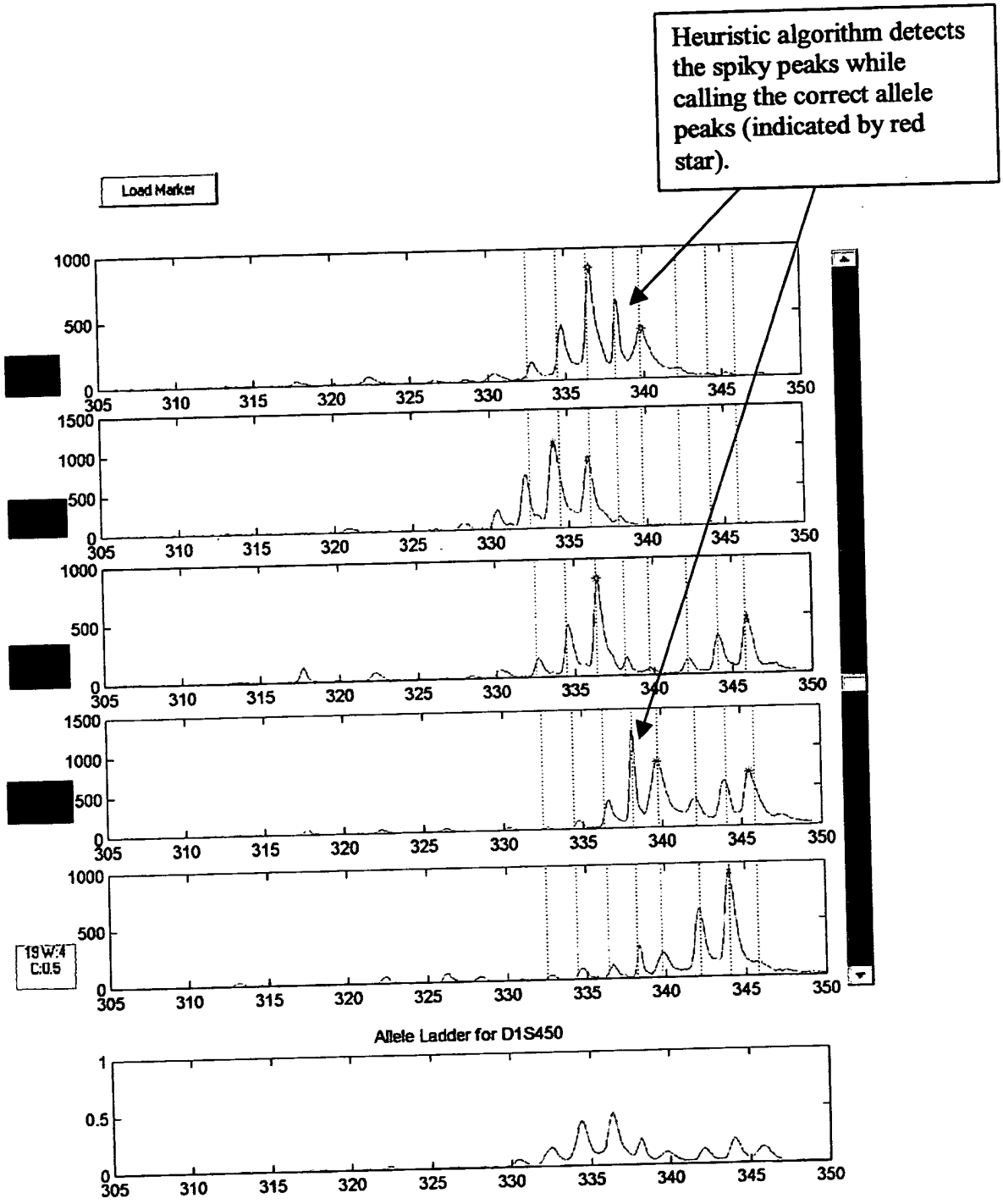

Figure 11

APPROVED BY DRAFTSMAN | O.G. FIG. | CLASS | SUBCLASS

Allele Calling for di-nucleotide marker in linkage mapping application Sample Data (1)

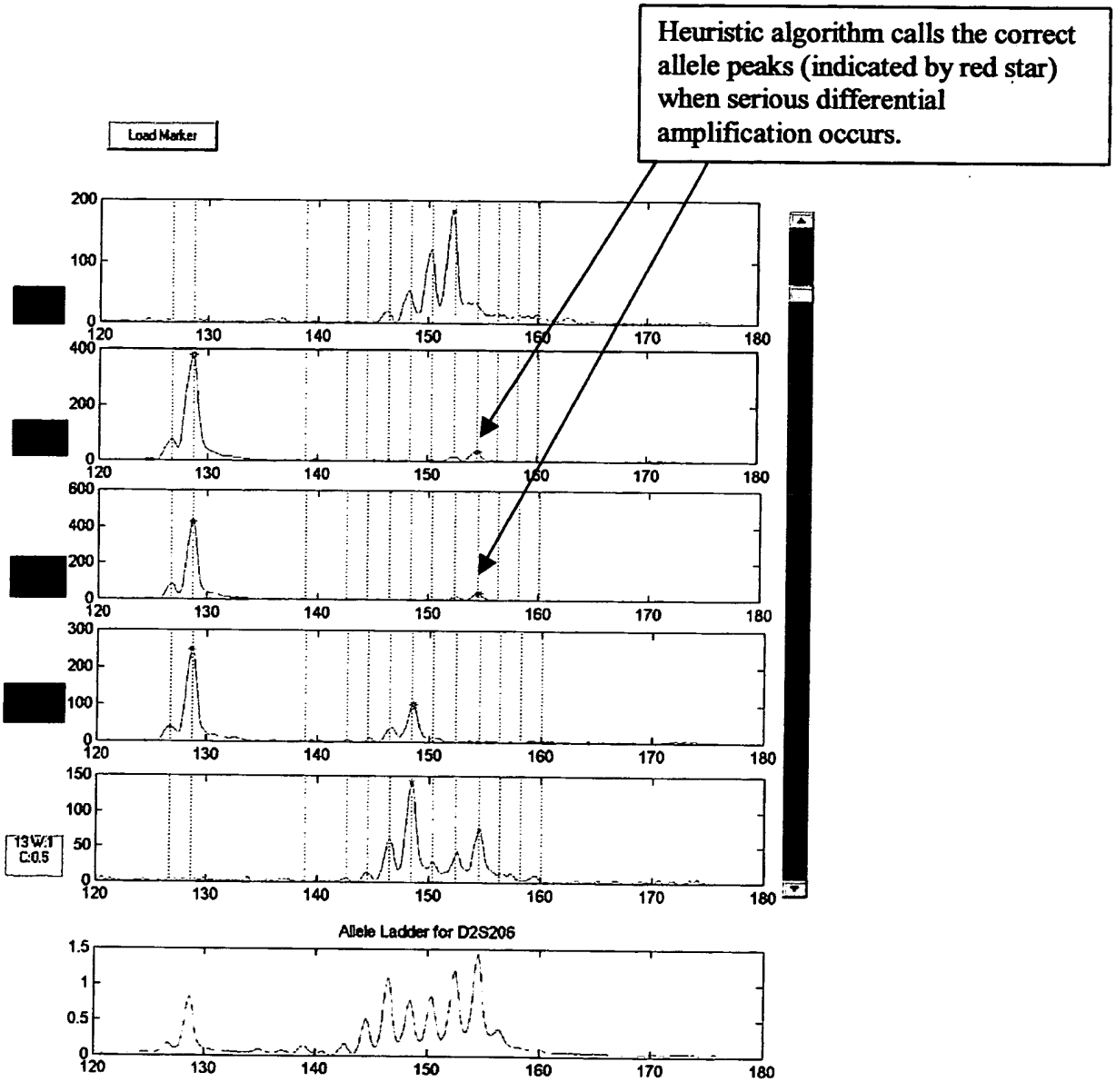

Figure 12

APPROVED BY DRAFTSMAN | O.G. FIG. | CLASS | SUBCLASS

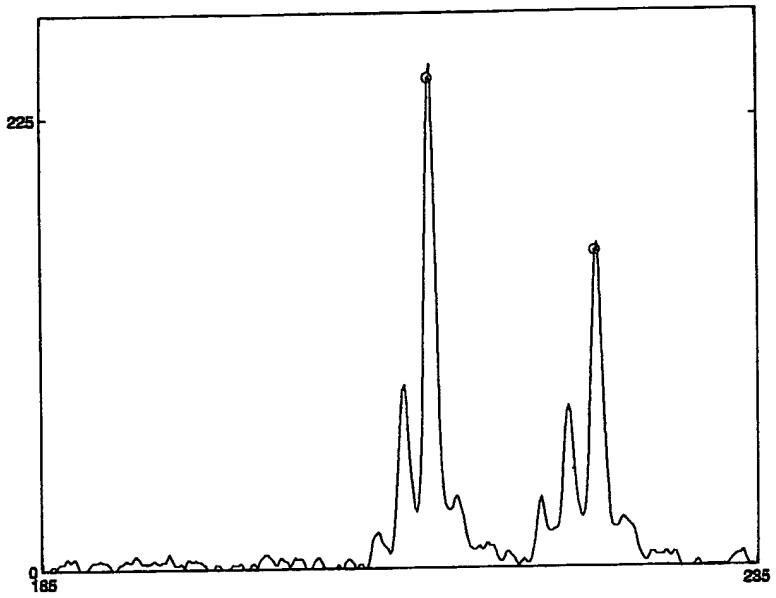

Figure 13: Standard heterozygous allele signature. Circles denote user annotated allele calls. x-axis is in base pairs. y-axis is in A/D counts (voltage intensity)

APPROVED BY DRAFTSMAN | O.G. FIG. | CLASS | SUBCLASS

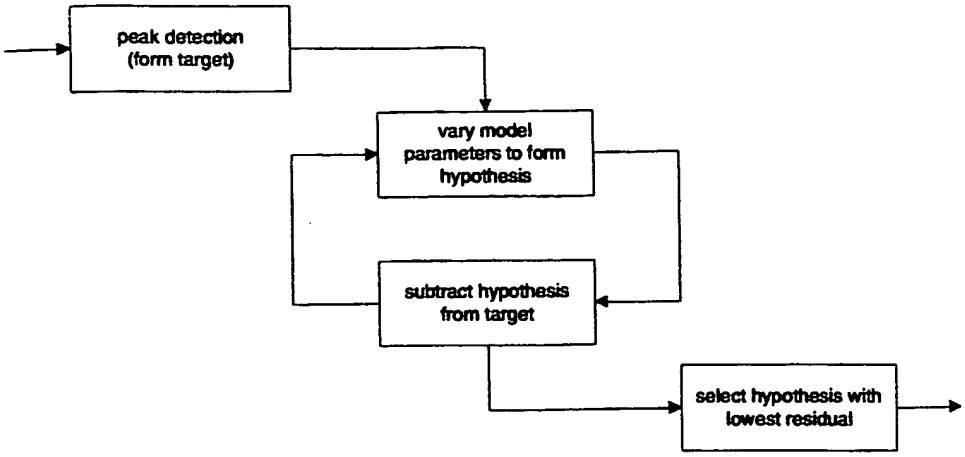

Figure 14: Steps in the allele calling routine. First the signal is simplified via sampling and its peaks are located. This forms the target signal that is to be approximated. The two interconnected boxes indicate the process of varying the parameters and testing how closely the resulting signal matches the sampled version of the original. The set of parameters that yield the closest match contain the allele calls.

APPROVED BY DRAFTSMAN | O G. FIG. | CLASS | SUBCLASS

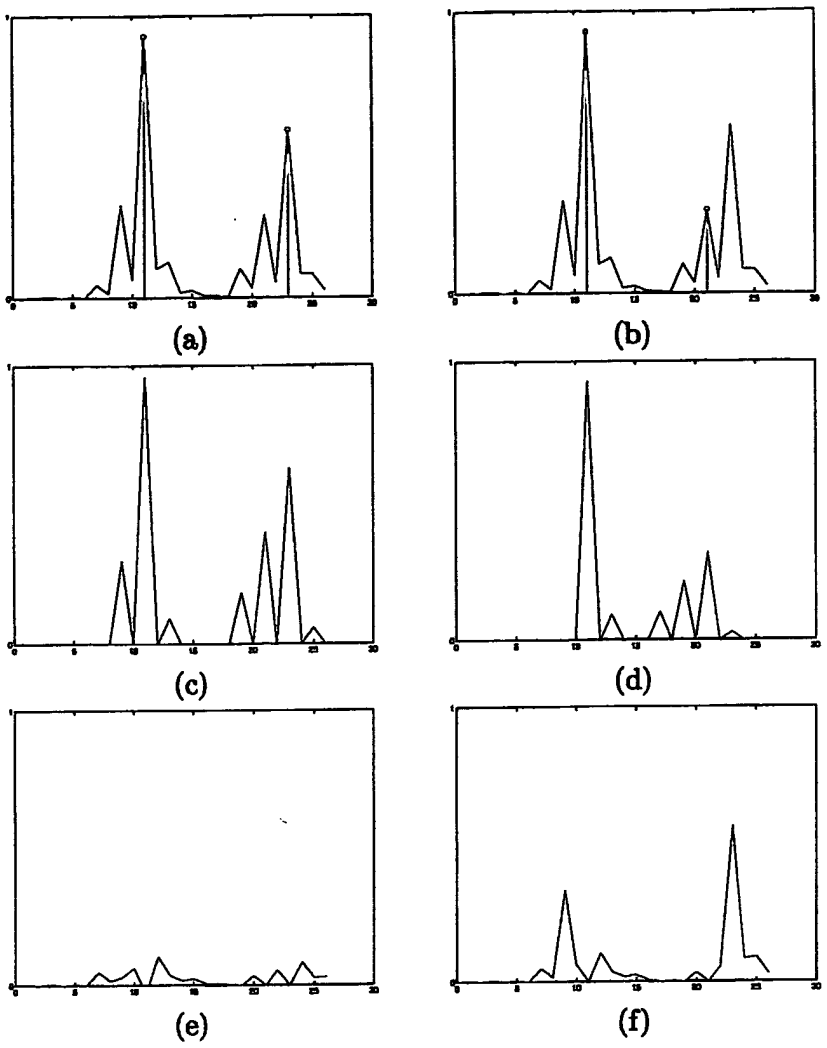

Figure 15: Illustration of hypothesis formation in the optimizer routine. The two columns of Figures represent the optimal solution (left column) and a suboptimal solution (right column). Panel (a) shows the target vector with the two red lines showing the location of the candidate peaks. Panel (c) shows the hypothesis formed using different values of stutter and $^{+}$A. Panel (c) shows the residual error resulting from subtraction of the signal in panel (c) from the signal in panel (a) (sum squared error = 0.0355). Panels (b,d,f) show the same process for for a slightly different allele hypothesis. This is a poor hypothesis and the residual is rather signifcant (SSE = 0.4715). The x-axis is somewhat meaningless at this point since it gets mapped back to base-pair indices after the winning hypothesis is chosen.

APPROVED BY DRAFTSMAN | O G. FIG. | CLASS | SUBCLASS

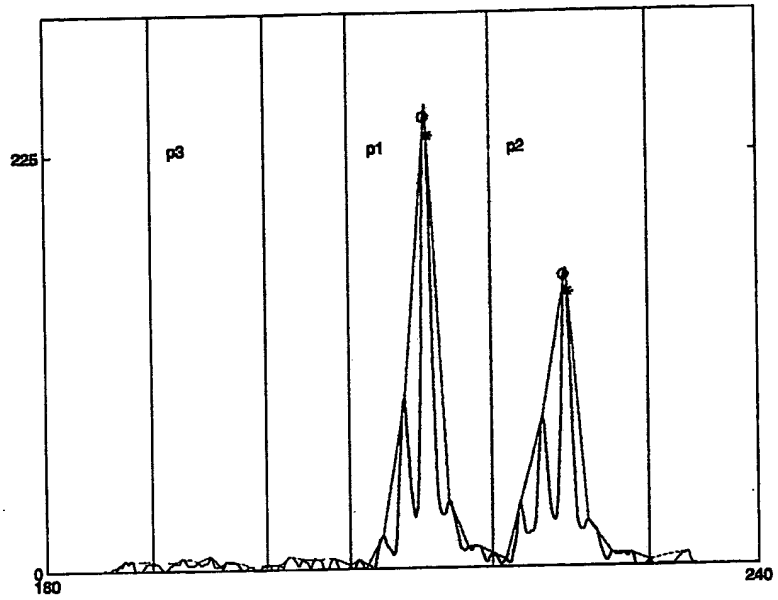

Figure 16: Division of heterozygous signal into panels by the Envelope Caller algorithm. The panels are ranked according to signal energy and the three of interest are labeled p1, p2 and p3 with the two panels containing strong allele signatures being shaded in blue. Circles denote user annotated allele calls. x-axis is in base pairs. y-axis is in A/D counts (voltage intensity)

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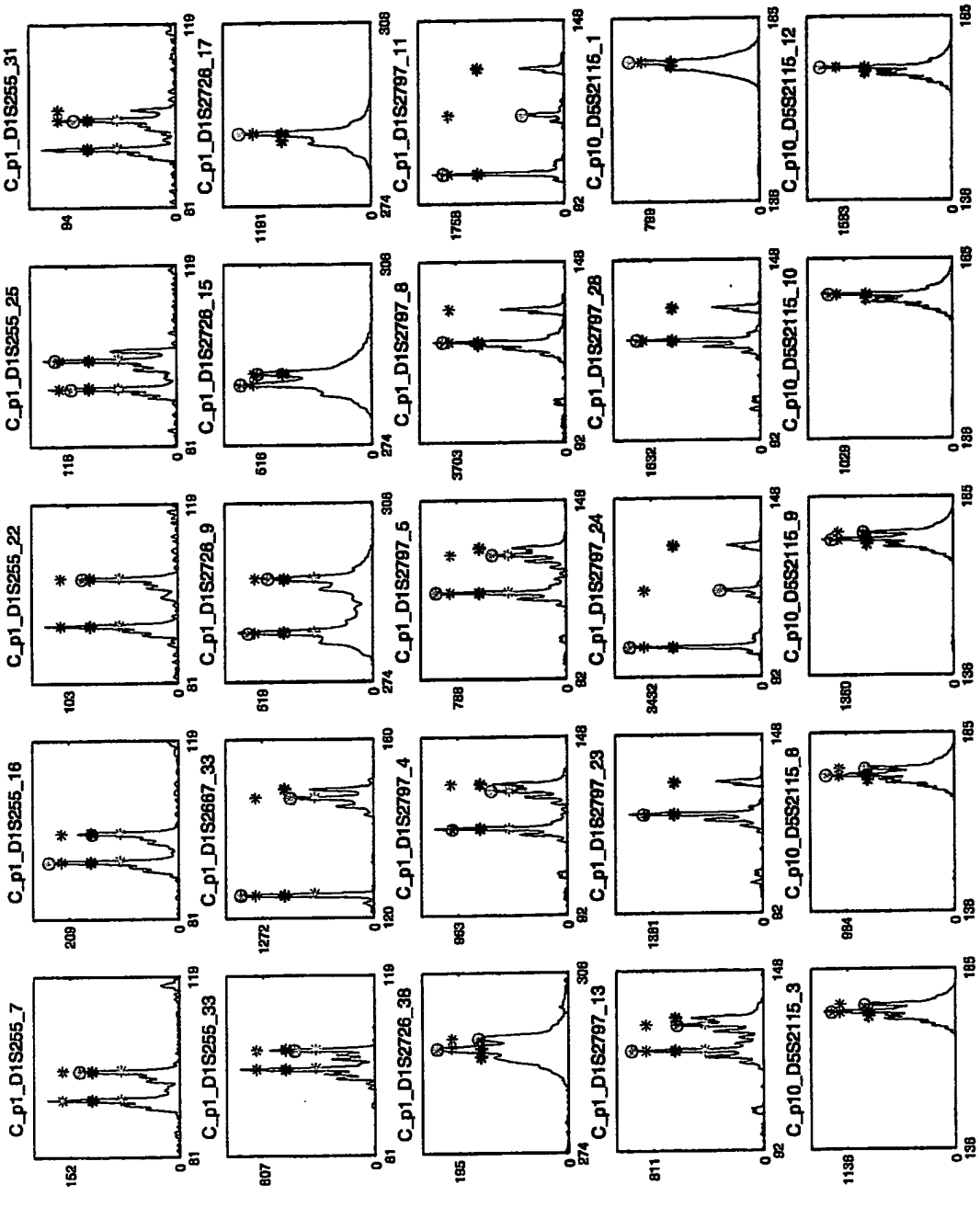

Figure 17: Example of how reporting could be accomplished. These are examples where consensus was not reached and show data that is difficult to interpret.